

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/358,103

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 _____ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/358,103

DATE: 07/30/1999
TIME: 12:05:22

Input Set: I358103.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Roca, Alberto I
2 <120> TITLE OF INVENTION: Mutants of Maw Motifs of RecA Protein Homologs, Methods
3 of Making Them, and Their Uses
4 <130> FILE REFERENCE: RecA Homolog Protein & Mutants
5 <140> CURRENT APPLICATION NUMBER: US/09/358,103
6 <141> CURRENT FILING DATE: 1999-07-21
7 <150> EARLIER APPLICATION NUMBER: 60/094,071
8 <151> EARLIER FILING DATE: 1998-07-24
9 <160> NUMBER OF SEQ ID NOS: 3
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 26
13 <212> TYPE: PRT
14 <213> ORGANISM: Escherichia coli
15 <220> FEATURE:
16 <221> NAME/KEY: NON_TER
17 <222> LOCATION: (1)
18 <220> FEATURE:
19 <221> NAME/KEY: NON_TER
20 <222> LOCATION: (26)..)
21 <220> FEATURE:
22 <221> NAME/KEY: HELIX
23 <222> LOCATION: (6)..(12)
24 <223> OTHER INFORMATION: Alpha-helix B
25 <220> FEATURE:
26 <221> NAME/KEY: STRAND
27 <222> LOCATION: (22)..(26)
28 <223> OTHER INFORMATION: Beta-strand 1
29 <220> FEATURE:
30 <221> NAME/KEY: SIMILAR
31 <222> LOCATION: (1)..(26)
32 <223> OTHER INFORMATION: This structure is highly conserved across
33 bacterial RecA and homologous eukaryotic,
34 archaeal, and viral proteins; sequence below is
35 from E. coli RecA positions 40-65
36 <400> SEQUENCE: 1
37 Ile Ser Thr Gly Ser Leu Ser Leu Asp Ile Ala Leu Gly Ala Gly Gly
38 1 5 10 15
39 Leu Pro Met Gly Arg Ile Val Glu Ile Tyr
40 20 25
41 <210> SEQ ID NO 2
42 <211> LENGTH: 26
43 <212> TYPE: PRT
44 <213> ORGANISM: Escherichia coli

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45 <220> FEATURE:
46 <221> NAME/KEY: NON_TER
47 <222> LOCATION: (1)
48 <220> FEATURE:
49 <221> NAME/KEY: NON_TER
50 <222> LOCATION: (26)
51 <220> FEATURE:
52 <221> NAME/KEY: HELIX
53 <222> LOCATION: (6)..(12)
54 <223> OTHER INFORMATION: Alpha-helix B
55 <220> FEATURE:
56 <221> NAME/KEY: STRAND
57 <222> LOCATION: (22)..(26)
58 <223> OTHER INFORMATION: Beta-strand 1
59 <220> FEATURE:
60 <221> NAME/KEY: SIMILAR
61 <222> LOCATION: (1)..(26)
62 <223> OTHER INFORMATION: Non 'Xaa' residues are the invariant MAW-motif
63 residues in RecA and its homologs
64 <400> SEQUENCE: 2

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what about the Xaa's

W--v 65 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly
66 1 5 10 15
W-- 67 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa
68 20 25

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69 <210> SEQ ID NO 3
70 <211> LENGTH: 26
71 <212> TYPE: PRT
72 <213> ORGANISM: Escherichia coli
73 <220> FEATURE:
74 <221> NAME/KEY: NON_TER
75 <222> LOCATION: (1)
76 <220> FEATURE:
77 <221> NAME/KEY: NON_TER
78 <222> LOCATION: (26)
79 <220> FEATURE:
80 <221> NAME/KEY: HELIX
81 <222> LOCATION: (6)..(12)
82 <223> OTHER INFORMATION: Alpha-helix B
83 <220> FEATURE:
84 <221> NAME/KEY: STRAND
85 <222> LOCATION: (22)..(26)
86 <223> OTHER INFORMATION: Beta-strand 1
87 <220> FEATURE:
88 <221> NAME/KEY: SIMILAR
89 <222> LOCATION: (1)..(26)

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90 <223> OTHER INFORMATION: Non "Xaa" residues are the invariant and
91 semiconservative elements of the MAW motif in RecA
92 and its homologs *same error*

93 <400> SEQUENCE: 3
94 Ile Xaa Thr Gly Xaa Xaa Xaa Leu Asp Xaa Ala Leu Xaa Xaa Gly Gly

15?? They
ly need to
be defined
(see item 10
on Even
summary
sheet)

in RecA
same error as above

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/358,103

DATE: 07/30/1999
TIME: 12:05:22

Input Set: I358103.RAW

	95		1						10		15
W-->	96	Leu	Xaa	Xaa	Gly	Xaa	Ile	Val	Glu	Ile	Tyr
	97				20				25		

VERIFICATION SUMMARY
PATENT APPLICATION US/09/358,103DATE: 07/30/1999
TIME: 12:05:22

Input Set: I358103.RAW

Line	Error/Warning	Original Text
65	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
67	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa
94	W "N" or "Xaa" used: Feature required	Ile Xaa Thr Gly Xaa Xaa Xaa Leu Asp Xaa A
96	W "N" or "Xaa" used: Feature required	Leu Xaa Xaa Gly Xaa Ile Val Glu Ile Tyr